

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Symbicom AB
- (B) STREET: Tvistevägen 48
- (C) CITY: Umeå
- (E) COUNTRY: Sweden
- (F) POSTAL CODE (ZIP): S-907 36

(ii) TITLE OF INVENTION: Pl3 antigens from Borrelia

(iii) NUMBER OF SEQUENCES: 31

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Borrelia burgdorferi
- (B) STRAIN: B313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Thr Ser Lys Gln Asp Pro Ile Val Pro Phe Leu Leu Asn Leu Phe Leu
1 5 10 15

Gly Phe Gly Ile Gly Ser Phe Ala Gln
20 25

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

09508487.031000

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ACNTCNAARC ARGAYCCNAT

20

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGNGCRAARC TNCCDATNCC

20

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACATCTAAGC AGGACCCTAT TGTACCATCT TTATTGAACC TTTTTTTAGG GTTTGGCATC

60

GGGAGCTTCG CCCA

74

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

09502497.031000

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGTACCATCT TTATTGAACC TTTTTTTAGG GTTT

34

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AAACCCTAAA AAAAGGTTCA ATAAAG

26

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GATTTTTCAT TGGATCCCAG AATTG

26

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

09508487 031000

26

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

21

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

31

(i) SEQUENCE CHARACTERISTICS:

SECRET

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGAATTCCTT GGTTCGCGT GGATCCATGA ATAACTTTT AATTTTGTGTT

50

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TAAAAAATT TAAAGAAAAG GAGGG

25

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGCTTATAGA ATCCGGGGCT TATTTGG

27

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

05508497 031000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TAGAATTCAG CAATTGCAAT ACAG

24

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CACCCATTTT CTAGATAAAT AAAATTAATA GC

32

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATAAAAGGTA CCATAGCTTT TTTTGAAAGA CAG

33

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

095048 031000

(A) ORGANISM: *Borrelia burgdorferi*
 (B) STRAIN: B31

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 170..709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

ATTGTTAAAA GAATTGAAAT TGATAATTTT ATGGTCAAAT CAAGAAGCTC TATTGGGAAG      60
CGAATTTCAA GCAATAATTT GAAAAAAGTT AAATTTAAAT AACTTTAAAA ACCTTTTTTTA      120
AATTTCATTA ATATGCTACC ATAGTACCAG TTTTAATAAA GGGGTTTTTT ATG AAT      175
                                         Met Asn
                                         1

AAA CTT TTA ATT TTT GTT TTG GCA ACC TTT TGT GTT TTT TCT AGC TTT      223
Lys Leu Leu Ile Phe Val Leu Ala Thr Phe Cys Val Phe Ser Ser Phe
      5              10              15

GCT CAA GCT AAT GAT TCT AAA AAT GGT GCG TTT GGG ATG AGT GCT GGA      271
Ala Gln Ala Asn Asp Ser Lys Asn Gly Ala Phe Gly Met Ser Ala Gly
      20              25              30

GAA AAA CTT TTG GTT TAT GAA ACT AGC AAG CAA GAT CCT ATT GTA CCA      319
Glu Lys Leu Leu Val Tyr Glu Thr Ser Lys Gln Asp Pro Ile Val Pro
      35              40              45              50

TTT TTA TTG AAC CTT TTT TTA GGG TTT GGA ATA GGC TCC TTT GCT CAA      367
Phe Leu Leu Asn Leu Phe Leu Gly Phe Gly Ile Gly Ser Phe Ala Gln
      55              60              65

GGA GAT ATT CTT GGA GGT TCT CTT ATT CTT GGA TTT GAT GCG GTT GGT      415
Gly Asp Ile Leu Gly Gly Ser Leu Ile Leu Gly Phe Asp Ala Val Gly
      70              75              80

ATA GGG CTT ATA CTT GCG GGG GCT TAT TTG GAT ATC AAA GCG CTT GAT      463
Ile Gly Leu Ile Leu Ala Gly Ala Tyr Leu Asp Ile Lys Ala Leu Asp
      85              90              95

GGT ATT ACT AAA AAA GCT GCT TTT CAA TGG ACT TGG GGT AAG GGA GTT      511
Gly Ile Thr Lys Lys Ala Ala Phe Gln Trp Thr Trp Gly Lys Gly Val

```

09503497-631000

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

```

Met Asn Lys Leu Leu Ile Phe Val Leu Ala Thr Phe Cys Val Phe Ser
  1                               5                               10                               15

Ser Phe Ala Gln Ala Asn Asp Ser Lys Asn Gly Ala Phe Gly Met Ser
      20                               25                               30

Ala Gly Glu Lys Leu Leu Val Tyr Glu Thr Ser Lys Gln Asp Pro Ile
      35                               40                               45

Val Pro Phe Leu Leu Asn Leu Phe Leu Gly Phe Gly Ile Gly Ser Phe

```


50 55 60

Ala Gln Gly Asp Ile Leu Gly Gly Ser Leu Ile Leu Gly Phe Asp Ala
65 70 75 80

Val Gly Ile Gly Leu Ile Leu Ala Gly Ala Tyr Leu Asp Ile Lys Ala
85 90 95

Leu Asp Gly Ile Thr Lys Lys Ala Ala Phe Gln Trp Thr Trp Gly Lys
100 105 110

Gly Val Met Leu Ala Gly Val Val Thr Met Ala Val Thr Arg Leu Thr
115 120 125

Glu Ile Ile Leu Pro Phe Thr Phe Ala Asn Ser Tyr Asn Arg Lys Leu
130 135 140

Lys Asn Ser Leu Asn Val Ala Leu Gly Gly Phe Glu Pro Ser Phe Asp
145 150 155 160

Val Ala Met Gly Gln Ser Ser Ala Leu Gly Phe Glu Leu Ser Phe Lys
165 170 175

Lys Ser Tyr
179

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 862 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Borrelia afzelii*
 - (B) STRAIN: ACAI
- (ix) FEATURE:

GATTTTTCAT TGGATCCCAG AATTTGTAGA ATTTTCGACA AATAAGACA TTATTAAAAG	60
AATTGAAATT GCTAATTTTA TGGTCAAATC AAGAAGCTCT ATTGGGAAGC GAATTTCAAG	120
TAATACTTTG AAAAAAGTTA AATTTAAATA GTTTTAAAAA CCTTTTTTTAA ATTTCATTA	180
TATGTTACTA TAATACCAGT TTTAATAAAG AGGTTTTT ATG AAT AAA TTT TTA	233
Met Asn Lys Phe ³ Leu	
1 5	
ATT GTT GTT TTG CTA GCC TTT TGT GTT TTT TCT AGC TTT GCT CAA GCT	281
Ile Val Val Leu Leu Ala Phe Cys Val Phe Ser Ser Phe Ala Gln Ala	
10 15 20	
GAT GAT TCT AAA AGC GCT TTT AAT TTG GGA GCG GGA GAA AAA CTT TTA	329
Asp Asp Ser Lys Ser Ala Phe Asn Leu Gly Ala Gly Glu Lys Leu Leu	
25 30 35	
GCT TAT GAA ACT AGT AAG AAA GAT CCT ATT GTG CCA TTT TTA TTG AAC	377
Ala Tyr Glu Thr Ser Lys Lys Asp Pro Ile Val Pro Phe Leu Leu Asn	
40 45 50	
CTT TTT TTA GGG TTT GGA ATA GGT TCT TTT GCT CAA GGA GAT ATT CTT	425
Leu Phe Leu Gly Phe Gly Ile Gly Ser Phe Ala Gln Gly Asp Ile Leu	
55 60 65	
GGG GGT TTT CTT ATT CTT GGA TTT GAT GCA GTT GGT ATA GGG TTA ATA	473
Gly Gly Phe Leu Ile Leu Gly Phe Asp Ala Val Gly Ile Gly Leu Ile	
70 75 80 85	
CTT ACA GGA GCT TAT TTA GAT ATC AAA GCT CTT GAT AAG AAT GCT CCA	521
Leu Thr Gly Ala Tyr Leu Asp Ile Lys Ala Leu Asp Lys Asn Ala Pro	
90 95 100	
AAA GCC GCT TTT AAG TGG ACT TGG GGT AAG GGA ATG ATG TTG GCA GGT	569
Lys Ala Ala Phe Lys Trp Thr Trp Gly Lys Gly Met Met Leu Ala Gly	
105 110 115	

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

ACA TTT GCT AAT AGT TAT AAT AGG AAA CTG AAA AAT AGC CTT AAT ATA 665
Thr Phe Ala Asn Ser Tyr Asn Arg Lys Leu Lys Asn Ser Leu Asn Ile
135 140 145

GCT TTT GGA GGG TTT GAG CCT AGT TTT GAT ATT AAT ATG GGC CAA GCT 713
Ala Phe Gly Gly Phe Glu Pro Ser Phe Asp Ile Asn Met Gly Gln Ala
150 155 160 165

AGC GCT CTT GGG TTT GAA CTA TCT TTC AAA AAA AGT TAT TAA 755
Ser Ala Leu Gly Phe Glu Leu Ser Phe Lys Lys Ser Tyr *
170 175

TTTTATTTTA TTATTAAAT GAGTGATAGC AATTTTGTAT TGTGATTGCT CATTGTAATT 815

GAAAATTAGA GCTTTTGTTT ATTATTTATA TTTTATTCT CTGCTAA 862

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met Asn Lys Phe Leu Ile Val Val Leu Leu Ala Phe Cys Val Phe Ser
1 5 10 15

Ser Phe Ala Gln Ala Asp Asp Ser Lys Ser Ala Phe Asn Leu Gly Ala
20 25 30

Gly Glu Lys Leu Leu Ala Tyr Glu Thr Ser Lys Lys Asp Pro Ile Val
35 40 45

Pro Phe Leu Leu Asn Leu Phe Leu Gly Phe Gly Ile Gly Ser Phe Ala

00000000000000000000000000000000

```

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 749 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Borrelia garinii
    (B) STRAIN: IP90

(ix) FEATURE:
    (A) NAME/KEY: CDS
  
```

(B) LOCATION:192..725

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 22:

TAGAATTTTC AACAAATAAA GATATTGTTA AAAGAATTGA AATTGCTAAT TTTATGGTTA	60
AATCAAGAAG CTCTATTGGT AAGCGAATTT CGAGTAACAA TTTGAAAAAA GTTAAATTTA	120
AATAGTTCCA AAAGCCTTTT TTAAATTTCA TTAATATGCT ACCATAATAC CAGTTTAATA	180
AAGGGGTTTT T ATG AAT AAG TTT TTA ATT TTT ATT TTG GTA ATC TTT TGT	230
Met Asn Lys Phe Leu Ile Phe Ile Leu Val Ile Phe Cys	
1 5 10	
GCT TTT TCT AGT TTT GCT CAA GAT GAT TCT AAA AGC ACT TTT AAT CTG	278
Ala Phe Ser Ser Phe Ala Gln Asp Asp Ser Lys Ser Thr Phe Asn Leu	
15 20 25	
GGA GCG GGA GAA AAA TTT TTG GTT TAT GAA ACT AAT AAG AAA GAT TCT	326
Gly Ala Gly Glu Lys Phe Leu Val Tyr Glu Thr Asn Lys Lys Asp Ser	
30 35 40 45	
CTT GTA CCA TTT TTA TTG AAC CTT TTT TTA GGG TTC GGG ATA GGT TCT	374
Leu Val Pro Phe Leu Leu Asn Leu Phe Leu Gly Phe Gly Ile Gly Ser	
50 55 60	
TTT GCT CAA GGA GAT ATC CTT GGA GGT TCT CTT ATT CTT GGA TTT GAT	422
Phe Ala Gln Gly Asp Ile Leu Gly Gly Ser Leu Ile Leu Gly Phe Asp	
65 70 75	
GCG GTT GGT ATA GGG TTA ATA CTT ACA GGA GCT TAT TTG GAC ATC AAG	470
Ala Val Gly Ile Gly Leu Ile Leu Thr Gly Ala Tyr Leu Asp Ile Lys	
80 85 90	
GAT TTT GAT AAT AAT GCT AAA AAA GCT GAT TTT AAG TGG ACT TGG GGT	518
Asp Phe Asp Asn Asn Ala Lys Lys Ala Asp Phe Lys Trp Thr Trp Gly	
95 100 105	
AAG GGA ATG ATG TTG GCA GGT GTG GTT ACT ATG GCT GTG ACA AGA TTG	566
Lys Gly Met Met Leu Ala Gly Val Val Thr Met Ala Val Thr Arg Leu	
110 115 120 125	

SECRET

AAA AAA AGC TAT TAA TTTTATTTAT CTAGAAAATG GGTG 749
Lys Lys Ser Tyr *
175

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Gly Asp Ile Leu Gly Gly Ser Leu Ile Leu Gly Phe Asp Ala Val Gly
65 70 75 80

Met Gly Gln Ala Ser Ala Leu Gly Phe Gly Leu Ser Phe Lys Lys Ser
165 170 175

(ii) MOLECULE TYPE: DNA (synthetic)

32

33

32

21

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

TTGCTTACAG AATTCGCTGG GCGAAACGAA

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 109...396
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 30:

ACGAGCTCAA	TCCAAACTTT	ATTGCTTGC	AATAAATTAA	TATTAATTTA	TTATAAATTG	60
CGCTAATATT	TTACTTGTCA	AAACTTACCA	TTAGGAGATA	ATAAAAAAC	ATG AAA AAA	117
					Met Lys Lys	
					1	
ATT TTC ACA TTA ATA TTA ATT TTT GGG TTG ACA ATT GAA ATC TTT GCC						165
Ile Phe Thr Leu Ile Leu Ile Phe Gly Leu Thr Ile Glu Ile Phe Ala						
5			10		15	
ACA AAA GAC ACA CAA AAT AGA ATT GAA AAA GGC ATT GAA AGT TTT AAC						213
Thr Lys Asp Thr Gln Asn Arg Ile Glu Lys Gly Ile Glu Ser Phe Asn						
20			25		30	35
AAA TAT GAT AAA GAG AAA AAA AAT CCA ATA GGG CCA TTC CTT TTA AAT						261
Lys Tyr Asp Lys Glu Lys Lys Asn Pro Ile Gly Pro Phe Leu Leu Asn						
		40			45	50
TTA TTT TTG CCC TTT GGA ATA GGA TCC TTT GTC CAA GGG GAT TAT ATT						309
Leu Phe Leu Pro Phe Gly Ile Gly Ser Phe Val Gln Gly Asp Tyr Ile						

55	60	65	
GGT GGA GGC TCA GTG CTT GGA TTT AAT TTA TTA GGA GCA ATC CTT TGG			357
Gly Gly Gly Ser Val Leu Gly Phe Asn Leu Leu Gly Ala Ile Leu Trp			
70	75	80	
GAA CTG GAA TTA TTC TTA ATC ACC GAG AAA CAC AAT TAA			396
Glu Leu Glu Leu Phe Leu Ile Thr Glu Lys His Asn			
85	90	95	

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met	Lys	Lys	Ile	Phe	Thr	Leu	Ile	Leu	Ile	Phe	Gly	Leu	Thr	Ile	Glu
1				5				10						15	
Ile	Phe	Ala	Thr	Lys	Asp	Thr	Gln	Asn	Arg	Ile	Glu	Lys	Gly	Ile	Glu
		20					25						30		
Ser	Phe	Asn	Lys	Tyr	Asp	Lys	Glu	Lys	Lys	Asn	Pro	Ile	Gly	Pro	Phe
		35					40						45		
Leu	Leu	Asn	Leu	Phe	Leu	Pro	Phe	Gly	Ile	Gly	Ser	Phe	Val	Gln	Gly
		50				55					60				
Asp	Tyr	Ile	Gly	Gly	Gly	Ser	Val	Leu	Gly	Phe	Asn	Leu	Leu	Gly	Ala
65					70					75					80
Ile	Leu	Trp	Glu	Leu	Glu	Leu	Phe	Leu	Ile	Thr	Glu	Lys	His	Asn	
				85					90					95	

09508487.034000